

Heatmap visualization of gene expression data across 100 samples. The color scale ranges from -2.0 (blue) to 2.0 (red). The dendrogram at the top shows hierarchical clustering of samples, with a color bar above it indicating sample groups: NC-3, MS-2, MS-3, MS-4, MS-5, MS-6, MS-7, MS-8, MS-9, MS-10, MS-11, MS-12, MS-13, MS-14, MS-15, MS-16, MS-17, MS-18, MS-19, MS-20, MS-21, MS-22, MS-23, MS-24, MS-25, MS-26, MS-27, MS-28, MS-29, MS-30, MS-31, MS-32, MS-33, MS-34, MS-35, MS-36, MS-37, MS-38, MS-39, MS-40, MS-41, MS-42, MS-43, MS-44, MS-45, MS-46, MS-47, MS-48, MS-49, MS-50, MS-51, MS-52, MS-53, MS-54, MS-55, MS-56, MS-57, MS-58, MS-59, MS-60, MS-61, MS-62, MS-63, MS-64, MS-65, MS-66, MS-67, MS-68, MS-69, MS-70, MS-71, MS-72, MS-73, MS-74, MS-75, MS-76, MS-77, MS-78, MS-79, MS-80, MS-81, MS-82, MS-83, MS-84, MS-85, MS-86, MS-87, MS-88, MS-89, MS-90, MS-91, MS-92, MS-93, MS-94, MS-95, MS-96, MS-97, MS-98, MS-99, MS-100. The heatmap shows a high degree of correlation between samples within each group, with a distinct shift in expression patterns between the two groups.

A hierarchical clustering dendrogram showing the relationship between various cancer types. The labels on the right include Lung, Pancreas, Breast, Prostate, Colorectal, Head&Neck, and Blood. The dendrogram uses black, green, and yellow lines to show the clustering hierarchy.

Supplemental Figure 2. Heatmap of miRNA precursor expression in 35 human cancer cell lines, filtered data. The names of the cancer cell lines are listed on the top of the figure. The relative expression of each gene was determined as described in Materials and Methods. Unsupervised hierarchical clustering was performed on a subset of 92 genes which are differentially expressed ($P = 0.01$) among groups of cell lines as determined by ANOVA multi-group comparison test. The heatmap color legend is on the top. B., dendrogram of clustering data with the class of cell lines listed.